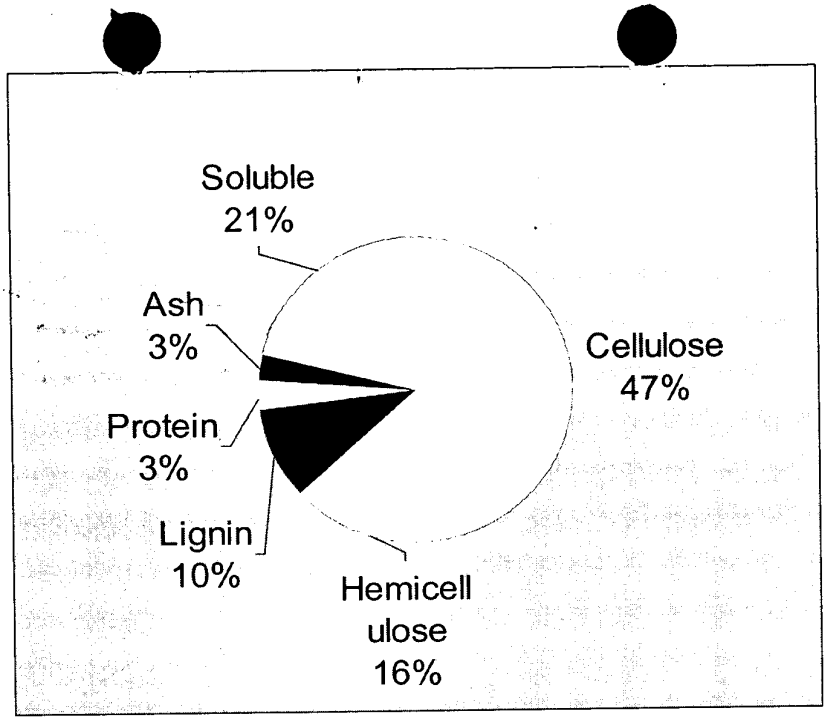

Figure 1.

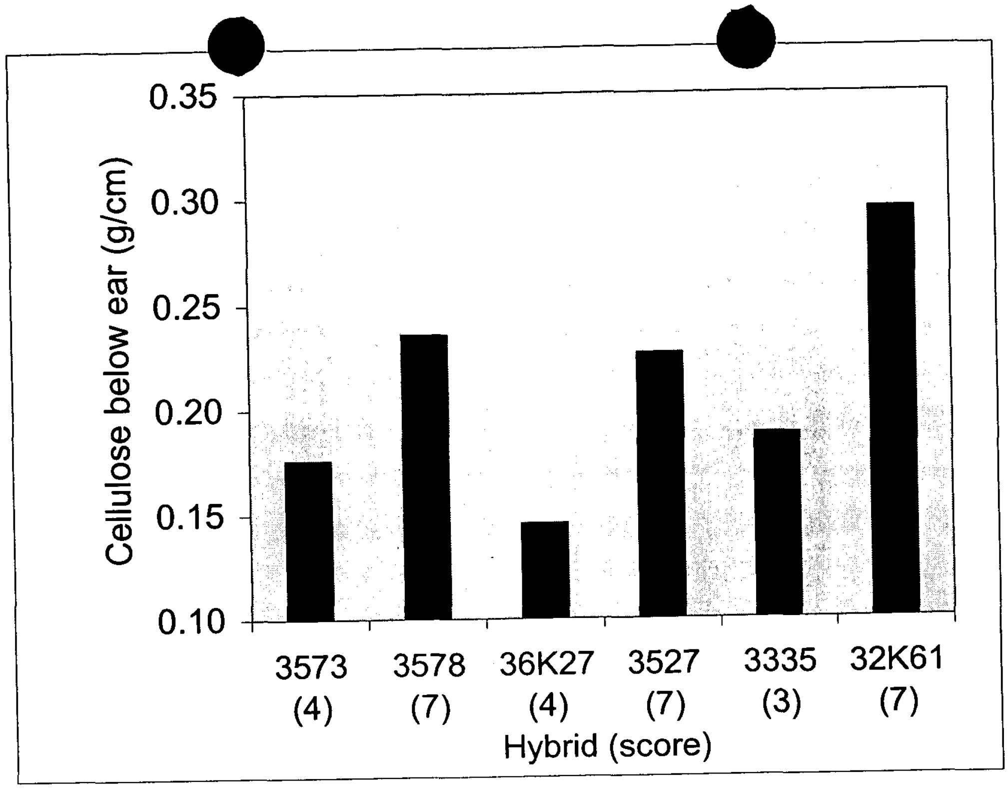

Figure 2

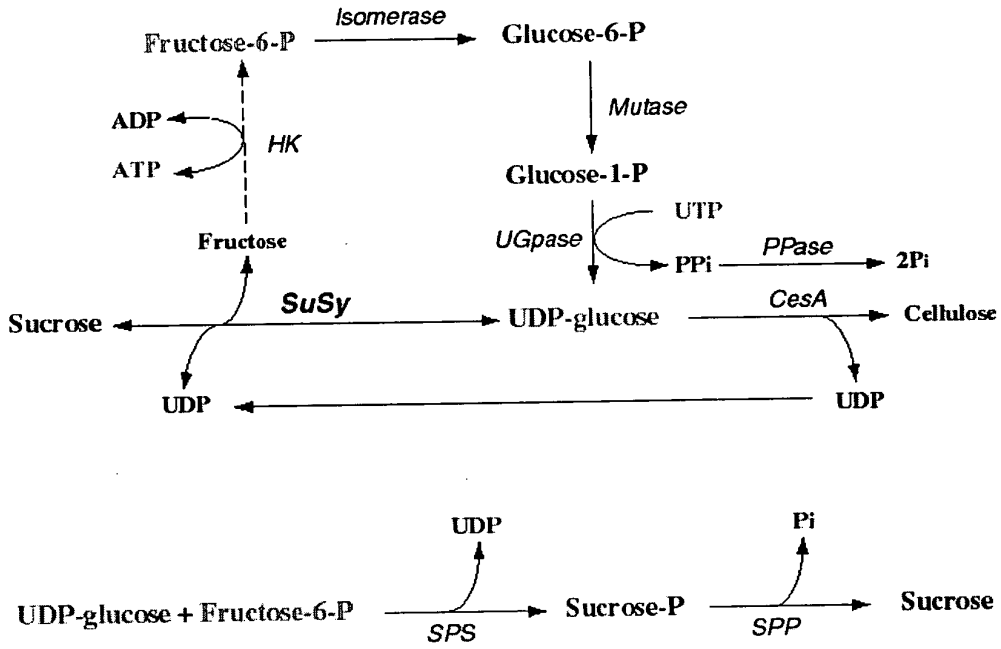

Figure 3.

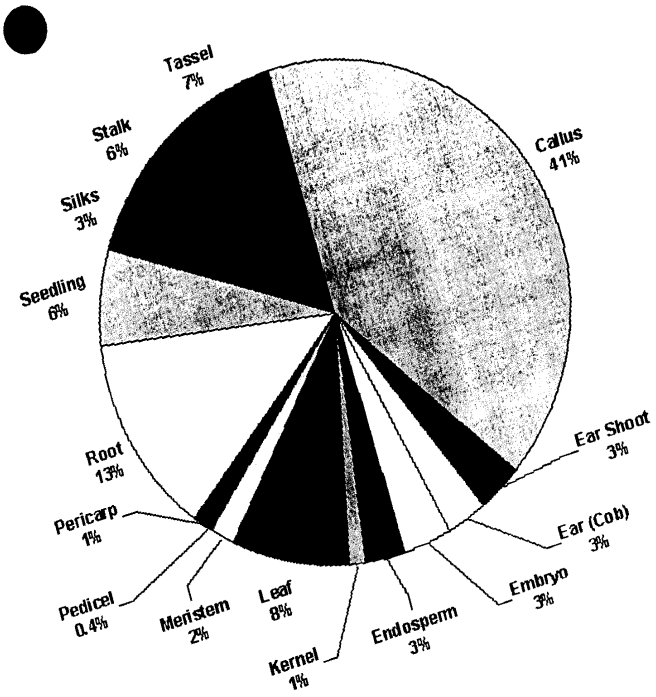

Figure 4.

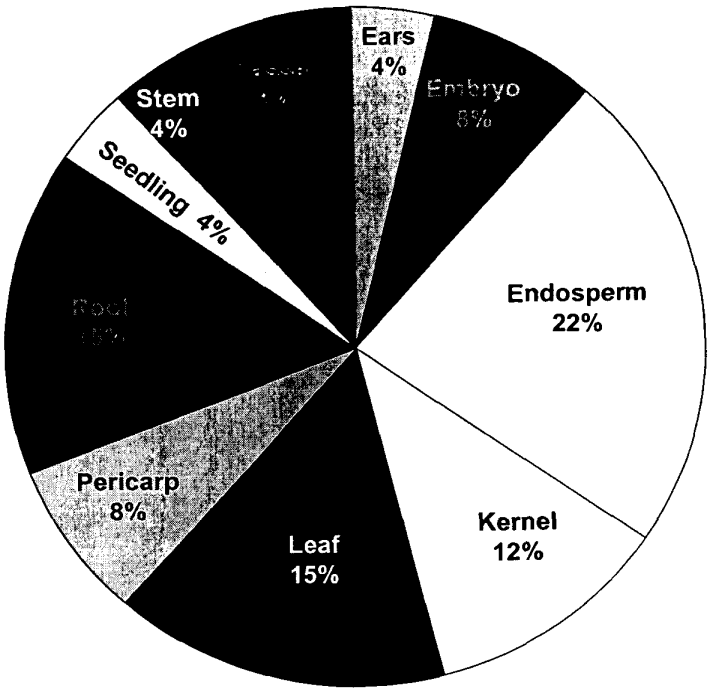

Figure 5

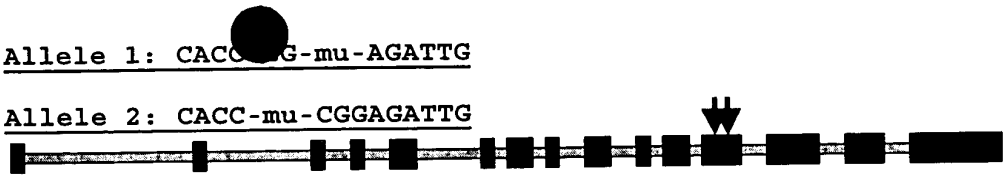

Figure 6.

Figure 7.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
Sus-1 (WT)	63.2	25.2 +/-0.38	39.9
sus-1 (mutant)	47.3	17.7 +/-0.34	37.4

```
                     1                                                50
      Sh1    (1)     -----MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVHQGKGMLQRHQ
     Sus1    (1)     MGEGAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLGKGMLQPHQ
     Sus3    (1)     -----------STHASGDRVEDTLHAHRNELVALLSKYVNKGKGILQPHH
Consensus    (1)               LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLQPHQ
                     51                                              100
      Sh1   (46)     LLAEFD-ALFDSDKE--KYAPFEDILRAAQEAIVLPPWVALAIRPRPGVW
     Sus1   (51)     ITAEYNNAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVW
     Sus3   (40)     ILDALDEVQGSGGRA-LAEGPFLDVLRSAQEAIVLPPFVAIAVRPRPGVW
Consensus   (51)     ILAEFD AI DADRE LKDGPFEDVLRAAQEAIVLPPWVALAIRPRPGVW
                     101                                             150
      Sh1   (93)     DYIRVNVSELAVEELSVSEYLAFKEQLVDGQSNSNFVLELDFEPFNASFP
     Sus1  (101)     EYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNFVLELDFEPFNASFP
     Sus3   (89)     EYVRVNVHELSVEQLTVSEYLRFKEELVDGQHNDPYVLELDFEPFNVSVP
Consensus  (101)     EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLELDFEPFNASFP
                     151                                             200
      Sh1  (143)     RPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNYKGTTMMLN
     Sus1  (151)     RPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLN
     Sus3  (139)     RPNRSSSIGNGVQFLNRHLSSIMFRNRDCLEPLLDFLRGHRHKGHVMMLN
Consensus  (151)     RPSLSKSIGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNYKG TMMLN
                     201                                             250
      Sh1  (193)     DRIQSLRGLQSSLRKAEEYILSVPQDTPYSEFNHRFQELGLEKGWGDTAK
     Sus1  (201)     DRIRSLSALQGALRKAEEHLSTLQADTPYSEFHHRFQELGLEKGWGDCAK
     Sus3  (189)     DRIQSLGRLQSVLTKAEEHISKLPADTPYSQFAYKFQEWGLEKGWGDTAG
Consensus  (201)     DRIQSL ALQSALRKAEEHLSSLPADTPYSEF HRFQELGLEKGWGDTAK
                     251                                             300
      Sh1  (243)     RVLDTLHLLLDLLEAPDPANLEKFLGTIPMMFNVVILSPHGYFAQSNVLG
     Sus1  (251)     RAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLG
     Sus3  (239)     HVLEMIHLLLDIIQAPDPSTLEKFLGRIPMIFNVVVVSPHGYFGQANVLG
Consensus  (251)     RVLETIHLLLDLLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG
                     301                                             350
      Sh1  (293)     YPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDAAGT
     Sus1  (301)     YPDTGGQVVYILDQVRAMENEMLLRIKQCGLDITPKILIVTRLLPDATGT
     Sus3  (289)     LPDTGGQIVYILDQVRALENEMVLRLKKQGLDVSPKILIVTRLIPDAKGT
Consensus  (301)     YPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDA GT
                     351                                             400
      Sh1  (343)     TCGQRLEKVIGTEHTDIIRVPFRNENGILRKWISRFDVWPYLETYTEDVS
     Sus1  (351)     TCGQRLEKVLGTEHCHILRVPFRTENGIVRKWISRFEVWPYLETYTDDVA
     Sus3  (339)     SCNQRLERISGTQHTYILRVPFRNENGILKKWISRFDVWPYLETFAEDAA
Consensus  (351)     TCGQRLEKVIGTEHTHILRVPFRNENGILRKWISRFDVWPYLETYTEDVA
                     401                                             450
      Sh1  (393)     SEIMKEMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPN
     Sus1  (401)     HEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPN
     Sus3  (389)     GEIAAELQGTPDFIIGNYSDGNLVASLLSYKMGITQCNIAHALEKTKYPD
Consensus  (401)      EIAAELQA PDLIIGNYSDGNLVASLLAHKMGVTQCTIAHALEKTKYPN
                     451                                             500
      Sh1  (443)     SDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYE
     Sus1  (451)     SDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYE
     Sus3  (439)     SDIFWKNFDEKYHFSCQFTADIIAMNNADFIITSTYQEIAGSKNTVGQYE
Consensus  (451)     SDIYWKKFDD YHFSCQFTADLIAMNHADFIITSTFQEIAGSKDTVGQYE
                     501                                             550
      Sh1  (493)     SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYYPYTETDKRLTAFH
     Sus1  (501)     SHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLH
     Sus3  (489)     SHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPHTEKAKRLTSLH
Consensus  (501)     SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTES KRLTSLH
```

Figure 8a

```
                    551                                                 600
      Sh1   (543)  PEIEELIYSDVENSEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGKN
      Sus1  (551)  PEIEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRN
      Sus3  (539)  GSIENLIYDPEQNDEHIGHLDDRSKPILFSMARLDRVKNITGLVEAFAKC
Consensus   (551)  PEIEELIYS  ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN

                    601                                                 650
      Sh1   (593)  ARLRELANLVIVAGDHGK-ESKDREEQAEFKKMYSLIDEYKLKGHIRWIS
      Sus1  (601)  KRLQELVNLVVVCGDHGN-PSKDKEEQAEFKKMFDLIEQYNLNGHIRWIS
      Sus3  (589)  AKLRELVNLVVVAGYNDVNKSKDREEIAEIEKMHELIKTHNLFGQFRWIS
Consensus   (601)  ARLRELVNLVVVAGDHG   SKDREEQAEFKKMHDLID YNL GHIRWIS
                    651                                                 700
      Sh1   (642)  AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVIESMTCGLPTIATCH
      Sus1  (650)  AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATAY
      Sus3  (639)  AQTNRARNGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLH
Consensus   (651)  AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFAT H
                    701                                                 750
      Sh1   (692)  GGPAEIIVDGVSGLHIDPYHSDKAADILVNFFDKCKADPSYWDEISQGGL
      Sus1  (700)  GGPAEIIVHGVSGYHIDPYQGDKASALLVDFFDKCQAEPSHWSKISQGGL
      Sus3  (689)  GGPAEIIEHGVSGFHIDPYHPEQAVNLMADFFDRCKQDPDHWVNISGAGL
Consensus   (701)  GGPAEIIVHGVSGFHIDPYH DKAA LLVDFFDKCKADPSHW  ISQGGL
                    751                                                 800
      Sh1   (742)  QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYIEMFYALKYR
      Sus1  (750)  QRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYR
      Sus3  (739)  QRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERLETRRYLEMFYILKFR
Consensus   (751)  QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR
                    801          817
      Sh1   (792)  SLASQVPLSFD------
      Sus1  (800)  TMASTVPLAVEGEPSSK
      Sus3  (789)  ELAKTVPLAID-QPQ--
Consensus   (801)  SLASTVPLAID  P
```

Figure 8b

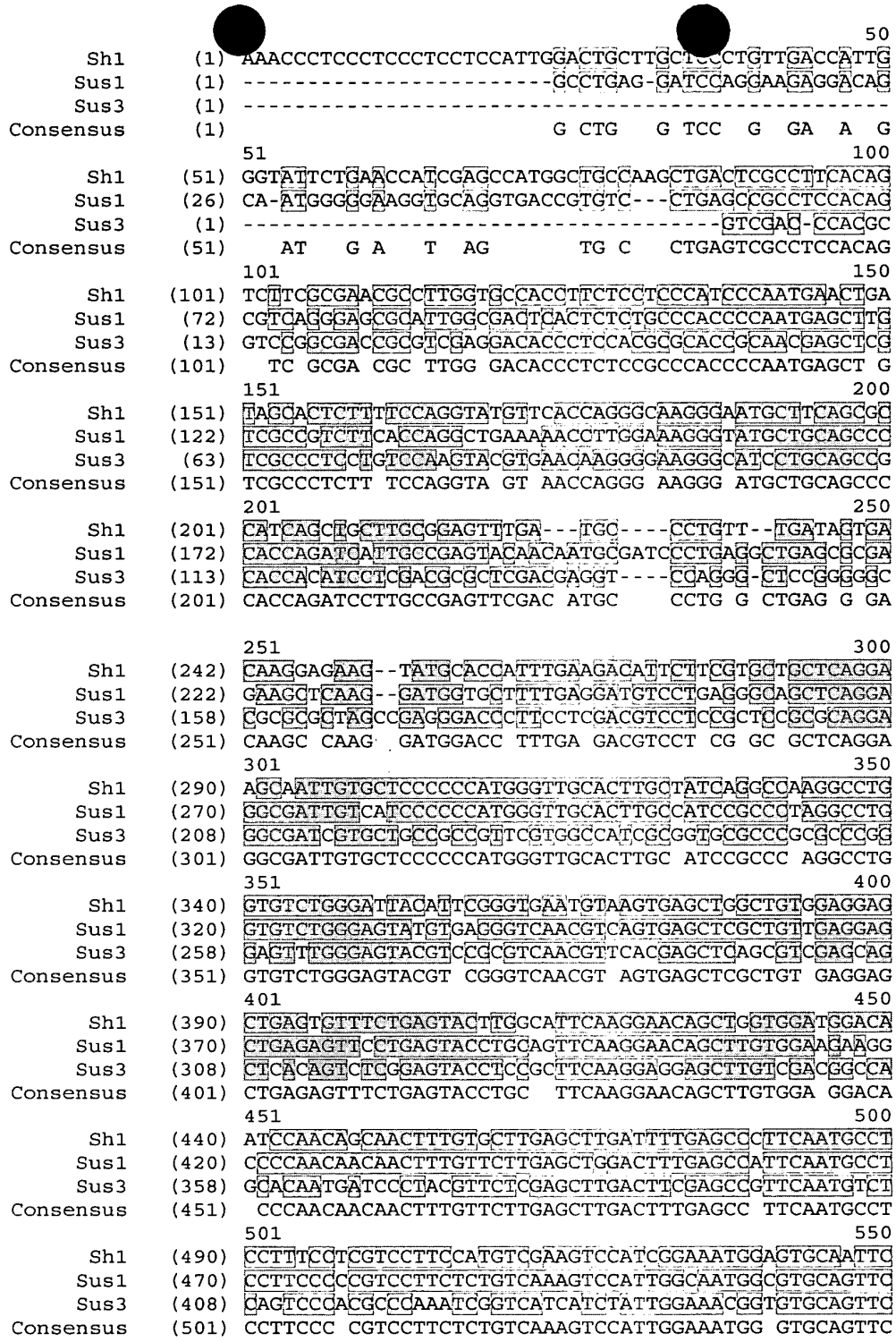
50
Sh1 (1) AAACCCTCCCTCCCTCCTCCATTGGACTGCTTGCTCCCTGTTGACCATTG
Sus1 (1) ----------GCCTGAG-GATCCAGCAAGAGGACAG
Sus3 (1) ----------
Consensus (1) G CTG G TCC G GA A G
51 100
Sh1 (51) GGTATTCTGAACCATCGAGCCATGGCTGCCAAGCTGACTCGCCTTCACAG
Sus1 (26) CA-ATGGGGGAAGGTGCAGGTGACCGTGTC---CTGAGCCGCCTCCACAG
Sus3 (1) ----------GTCGAG-CCACGC
Consensus (51) AT G A T AG TG C CTGAGTCGCCTCCACAG
101 150
Sh1 (101) TCTTCGCGAACGCCTTGGTGCCACCTTCTCCTCCCATCCCAATGAACTGA
Sus1 (72) CGTCAGGGAGCGCATTGGCGACTCACTCTCTGCCCACCCCAATGAGCTTG
Sus3 (13) GTCCGGCGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGCTCG
Consensus (101) TC GCGA CGC TTGG GACACCCTCTCCGCCCACCCCAATGAGCT G
151 200
Sh1 (151) TAGCACTCTTTTCCAGGTATGTTCACCAGGGCAAGGGAATGCTTCAGCGC
Sus1 (122) TCGCCGTCTTCACCAGGCTGAAAAACCTTGGAAAGGGTATGCTGCAGCCC
Sus3 (63) TCGCCCTCCTGTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCG
Consensus (151) TCGCCCTCTT TCCAGGTA GT AACCAGGG AAGGG ATGCTGCAGCCC
201 250
Sh1 (201) CATCAGCTGCTTGCGGAGTTTGA---TGC----CCTGTT--TGATAGTGA
Sus1 (172) CACCAGATCATTGCCGAGTACAACAATGCGATCCCTGAGGCTGAGCGCGA
Sus3 (113) CACCACATCCTCGACGCGCTCGACGAGGT----CCAGGG-CTCCGGGGGC
Consensus (201) CACCAGATCCTTGCCGAGTTCGAC ATGC CCTG G CTGAG G GA
251 300
Sh1 (242) CAAGGAGAAG--TATGCACCATTTGAAGACATTCTTCGTGCTGCTCAGGA
Sus1 (222) GAAGCTCAAG--GATGGTGCTTTTGAGGATGTCCTGAGGGCAGCTCAGGA
Sus3 (158) CGCGCGCTAGCCGAGGGACCCTTCCTCGACGTCCTCCGCTCCGCGCAGGA
Consensus (251) CAAGC CAAG GATGGACC TTTGA GACGTCCT CG GC GCTCAGGA
301 350
Sh1 (290) AGCAATTGTGCTCCCCCCATGGGTTGCACTTGCTATCAGGCCAAGGCCTG
Sus1 (270) GGCGATTGTCATCCCCCCATGGGTTGCACTTGCCATCCGCCCTAGGCCTG
Sus3 (208) GGCGATCGTGCTGCCGCCGTTCGTGGCCATCGCGGTGCGCCCGCGCCCGG
Consensus (301) GGCGATTGTGCTCCCCCCATGGGTTGCACTTGC ATCCGCCC AGGCCTG
351 400
Sh1 (340) GTGTCTGGGATTACATTCGGGTGAATGTAAGTGAGCTGGCTGTGGAGGAG
Sus1 (320) GTGTCTGGGAGTATGTGAGGGTCAACGTCAGTGAGCTCGCTGTTGAGGAG
Sus3 (258) GAGTTTGGGAGTACGTCCGCGTCAACGTTCACGAGCTCAGCGTCGAGCAG
Consensus (351) GTGTCTGGGAGTACGT CGGGTCAACGT AGTGAGCTCGCTGT GAGGAG
401 450
Sh1 (390) CTGAGTGTTTCTGAGTACTTGGCATTCAAGGAACAGCTGGTGGATGGACA
Sus1 (370) CTGAGAGTTCCTGAGTACCTGCAGTTCAAGGAACAGCTTGTGGAAGAAGG
Sus3 (308) CTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTTGTCGACGGCCA
Consensus (401) CTGAGAGTTTCTGAGTACCTGC TTCAAGGAACAGCTTGTGGA GGACA
451 500
Sh1 (440) ATCCAACAGCAACTTTGTGCTTGAGCTTGATTTTGAGCCCTTCAATGCCT
Sus1 (420) CCCCAACAACAACTTTGTTCTTGAGCTGGACTTTGAGCCATTCAATGCCT
Sus3 (358) GCACAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCCGTTCAATGTCT
Consensus (451) CCCAACAACAACTTTGTTCTTGAGCTTGACTTTGAGCC TTCAATGCCT
501 550
Sh1 (490) CCTTTCCTCGTCCTTCCATGTCGAAGTCCATCGGAAATGGAGTGCAATTC
Sus1 (470) CCTTCCCCCGTCCTTCTCTGTCAAAGTCCATTGGCAATGGCGTGCAGTTC
Sus3 (408) CAGTCCCACGCCCAAATCGGTCATCATCTATTGGAAACGGTGTGCAGTTC
Consensus (501) CCTTCCC CGTCCTTCTCTGTCAAAGTCCATTGGAAATGG GTGCAGTTC

Figure 9a

```
                     551                                              600
Sh1          (540)   CTTAACCGACACCTGTCGTCCAAGTTGTTCCAGGACAAGGAGAGTTTGTA
Sus1         (520)   CTCAACAGGCACCTGTCATCAAAGCTCTTCCATGACAAGGAGAGCATGTA
Sus3         (458)   CTCAACCGACACTTGTCCTCAATCATGTTCCGCAACAGGGATTGCTTGGA
Consensus    (551)   CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGTA
                     601                                              650
Sh1          (590)   CCCCTTGCTGAACTTCCTCAAGGCTCATAACTACAAGGGCACGACGATGA
Sus1         (570)   CCCCTTGCTCAACTTCCTTCGCGCCCACAACTACAAGGGGATGACCATGA
Sus3         (508)   GCCCCTGTTGGATTTCCTCCGTGGCCACCGGCACAAGGGGCATGTTATGA
Consensus    (601)   CCCCTTGCTGAACTTCCTCCG GCCCACAACTACAAGGGGA GAC ATGA
                     651                                              700
Sh1          (640)   TGTTGAATGACAGAATCCAAAGCCTTCGTGGTCTCCAATCATCCCTGAGA
Sus1         (620)   TGTTGAACGACAGAATCCGCAGTCTCAGTGCTCTGCAAGGTGCGCTGAGG
Sus3         (558)   TGCTTAATGATAGAATACAAAGCTTGGGAGGCTTCAGTCTGTGCTGACC
Consensus    (651)   TGTTGAATGACAGAATCCAAAGCCT  GTGGTCT CAATCTGCGCTGAG
                     701                                              750
Sh1          (690)   AAGGCAGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA
Sus1         (670)   AAGGCTGAGGAGCACCTGTCCACCCTACAAGCTGATACCCCATACTCTGA
Sus3         (608)   AAAGCTGAGGAGCACTTGTCAAAGCTCCCTGCTGACACACCATACTCACA
Consensus    (701)   AAGGCTGAGGAGCACCTGTC A  CT CCTGCTGACAC CCATACTC GA
                     751                                              800
Sh1          (740)   GTTCAACCATAGGTTCCAAGAGCTTGGCTTGGAGAAGGGTTGGGGTGACA
Sus1         (720)   ATTTCACCACAGGTTCCAGGAACTTGGTCTGGAGAAGGGTTGGGGTGATT
Sus3         (658)   ATTTGCTTATAAATTTCAAGAGTGGGGCCTGGAGAAAGGTTGGGGTGATA
Consensus    (751)   ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGGTTGGGGTGATA
                     801                                              850
Sh1          (790)   CTGCGAAGCGTGTTCTCGACACACTCCACTTGCTTCTCGACCTTCTTGAG
Sus1         (770)   GCGCTAAGCGTGCACAGGAGACTATCCACCTCCTCTTGGACCTCCTGGAG
Sus3         (708)   CAGCAGGACATGTTTTGGAAATGATCCATCTCCTTCTAGACATCATTCAG
Consensus    (801)   C GC AAGCGTGTTCTGGA AC ATCCACCTCCTTCT GACCTCCTTGAG
                     851                                              900
Sh1          (840)   GCCCCTGATCCTGCCAACTTGGAGAAGTTCCTTGGAACTATACCAATGAT
Sus1         (820)   GCCCCAGATCCGTCCACCCTGGAGAAGTTCCTTGGAACGATCCCCATGGT
Sus3         (758)   GCGCCAGACCCATCTACCCTAGAGAAATTCTTGGGGAGGATCCCCATGAT
Consensus    (851)   GCCCCAGATCC TCCACCCTGGAGAAGTTCCTTGGAACGATCCCCATGAT
                     901                                              950
Sh1          (890)   GTTCAACGTTGTTATCCTGTCTCCTCATGGCTACTTCGCCCAGTCCAATG
Sus1         (870)   GTTCAATGTCGTTATCCTCTCCCCTCATGGTTACTTCGCTCAAGCTAATG
Sus3         (808)   TTTTAACGTTGTTGTGGTATCCCCTCATGGATACTTTGGTCAAGCTAATG
Consensus    (901)   GTTCAACGTTGTTATCCT TCCCCTCATGG TACTTCGCTCAAGCTAATG
                     951                                             1000
Sh1          (940)   TGCTTGGATACCCTGACACTGGCGGTCAGGTTGTGTACATTCTGGATCAA
Sus1         (920)   TCTTGGGTTACCCTGACACCGGAGGCCAGGTTGTCTACATCTTGGATCAA
Sus3         (858)   TATTAGGCTTGCCAGACACAGGAGGACAGATCGTCTATATACTGGACCAA
Consensus    (951)   T TT GG TACCCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA
                     1001                                            1050
Sh1          (990)   GTCCGTGCTTTGGAGAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCCT
Sus1         (970)   GTGCGCGCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGGTCT
Sus3         (908)   GTCCGTGCACTAGAAAATGAGATGGTTCTCCGTTTAAAGAAACAAGGGCT
Consensus   (1001)   GTCCGTGCT TGGAGAATGAGATGCTTCTGAGGAT AAGCAGCAAGG CT
                     1051                                            1100
Sh1         (1040)   TGATATCACTCCGAAGATCCTCATTGTTACCAGGCTGTTGCCTGATGCTG
Sus1        (1020)   TGACATCACGCCGAAGATCCTTATTGTCACCAGGTTGCTCCCTGATGCAA
Sus3         (958)   TGATGTTTCCCCAAAGATTCTCATTGTTACTCGGCTGATACCAGATGCAA
Consensus   (1051)   TGATATCAC CCGAAGATCCTCATTGTTACCAGGCTG T CCTGATGCAA
```

Figure 9b

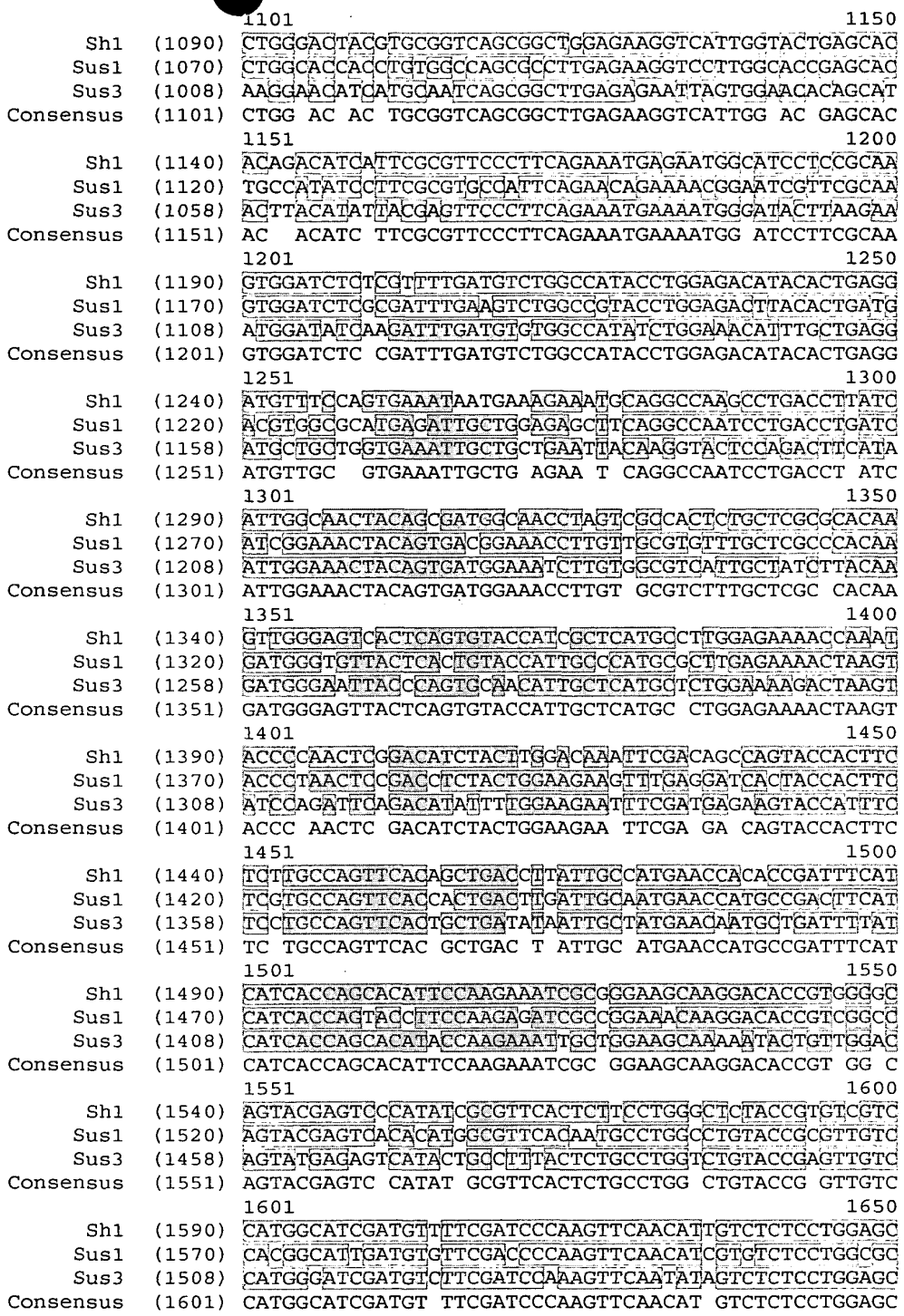
1101 1150
Sh1 (1090) CTGGGACTACGTGCGGTCAGCGGCTGGAGAAGGTCATTGGTACTGAGCAC
Sus1 (1070) CTGGCACCACCTGTGGCCAGCGCCTTGAGAAGGTCCTTGGCACCGAGCAC
Sus3 (1008) AAGGAACATCATGCAATCAGCGGCTTGAGAGAATTAGTGGAACACAGCAT
Consensus (1101) CTGG AC AC TGCGGTCAGCGGCTTGAGAAGGTCATTGG AC GAGCAC
1151 1200
Sh1 (1140) ACAGACATCATTCGCGTTCCCTTCAGAAATGAGAATGGCATCCTCCGCAA
Sus1 (1120) TGCCATATCCTTCGCGTGCCATTCAGAACAGAAAACGGAATCGTTCGCAA
Sus3 (1058) ACTTACATATTACGAGTTCCCTTCAGAAATGAAAATGGGATACTTAAGAA
Consensus (1151) AC ACATC TTCGCGTTCCCTTCAGAAATGAAAATGG ATCCTTCGCAA
1201 1250
Sh1 (1190) GTGGATCTCTCGTTTTGATGTCTGGCCATACCTGGAGACATACACTGAGG
Sus1 (1170) GTGGATCTCGCGATTTGAAGTCTGGCCGTACCTGGAGACTTACACTGATG
Sus3 (1108) ATGGATATCAAGATTTGATGTGTGGCCATATCTGGAAACATTTGCTGAGG
Consensus (1201) GTGGATCTC CGATTTGATGTCTGGCCATACCTGGAGACATACACTGAGG
1251 1300
Sh1 (1240) ATGTTTCCAGTGAAATAATGAAAGAAATGCAGGCCAAGCCTGACCTTATC
Sus1 (1220) ACGTGGCGCATGAGATTGCTGGAGAGCTTCAGGCCAATCCTGACCTGATC
Sus3 (1158) ATGCTGCTGGTGAAATTGCTGCTGAATTACAAGGTACTCCAGACTTCATA
Consensus (1251) ATGTTGC GTGAAATTGCTG AGAA T CAGGCCAATCCTGACCT ATC
1301 1350
Sh1 (1290) ATTGGCAACTACAGCGATGGCAACCTAGTCGCCACTCTGCTCGCGCACAA
Sus1 (1270) ATCGGAAACTACAGTGACGGAAACCTTGTTGCGTGTTTGCTCGCCCACAA
Sus3 (1208) ATTGGAAACTACAGTGATGGAAATCTTGTGGCGTCATTGCTATCTTACAA
Consensus (1301) ATTGGAAACTACAGTGATGGAAACCTTGT GCGTCTTTGCTCGC CACAA
1351 1400
Sh1 (1340) GTTGGGAGTCACTCAGTGTACCATCGCTCATGCCTTGGAGAAAACCAAAT
Sus1 (1320) GATGGGTGTTACTCACTGTACCATTGCCCATGCGCTTGAGAAAACTAAGT
Sus3 (1258) GATGGGAATTACCCAGTGCAACATTGCTCATGCTCTGGAAAAGACTAAGT
Consensus (1351) GATGGGAGTTACTCAGTGTACCATTGCTCATGC CTGGAGAAAACTAAGT
1401 1450
Sh1 (1390) ACCCCAACTCGGACATCTACTTGGACAAATTCGACAGCCAGTACCACTTC
Sus1 (1370) ACCCTAACTCCGACCTCTACTGGAAGAAGTTTGAGGATCACTACCACTTC
Sus3 (1308) ATCCAGATTCAGACATATTTTGGAAGAATTTCGATGAGAAGTACCATTTC
Consensus (1401) ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC
1451 1500
Sh1 (1440) TCTTGCCAGTTCACAGCTGACCTTATTGCCATGAACCACACCGATTTCAT
Sus1 (1420) TCGTGCCAGTTCACCACTGACTTGATTGCAATGAACCATGCCGACTTCAT
Sus3 (1358) TCCTGCCAGTTCACTGCTGATATAATTGCTATGAACAATGCTGATTTTAT
Consensus (1451) TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTCAT
1501 1550
Sh1 (1490) CATCACCAGCACATTCCAAGAAATCGCGGGAAGCAAGGACACCGTGGGGC
Sus1 (1470) CATCACCAGTACCTTCCAAGAGATCGCCGGAAACAAGGACACCGTCGGCC
Sus3 (1408) CATCACCAGCACATACCAAGAAATTGCTGGAAGCAAAAATACTGTTGGAC
Consensus (1501) CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C
1551 1600
Sh1 (1540) AGTACGAGTCCCATATCGCGTTCACTCTTCCTGGGCTCTACCGTGTCGTC
Sus1 (1520) AGTACGAGTCACACATGGCGTTCACAATGCCTGGCCTGTACCGCGTTGTC
Sus3 (1458) AGTATGAGAGTCATACTGCCTTTACTCTGCCTGGTCTGTACCGAGTTGTC
Consensus (1551) AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC
1601 1650
Sh1 (1590) CATGGCATCGATGTTTTCGATCCCAAGTTCAACATTGTCTCTCCTGGAGC
Sus1 (1570) CACGGCATTGATGTGTTCGACCCCAAGTTCAACATCGTGTCTCCTGGCGC
Sus3 (1508) CATGGGATCGATGTCTTCGATCCAAAGTTCAATATAGTCTCTCCTGGAGC
Consensus (1601) CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCCTGGAGC

Figure 9c

```
                      1651                                              1700
      Sh1    (1640)  AGACATGAGTGTTTACTACCCTTATACGGAAACCGACAAGAGACTCACTG
     Sus1    (1620)  GGACCTGTCCATCTACTTCCCGTACACCGAGTCGCACAAGAGGCTGACCT
     Sus3    (1558)  TGACATGTCCATATACTTTCCACATACCGAGAAGGCCAAGCGACTCACCT
Consensus    (1651)   GACATGTCCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT

                      1701                                              1750
      Sh1    (1690)  CCTTCCATCCTGAAATCGAGGAGCTCATCTACAGCGACGTCGAGAACTCC
     Sus1    (1670)  CCCTTCACCCGGAGATTGAGGAGCTCCTGTACAGCCAAACCGAGAACACG
     Sus3    (1608)  CTCTTCATGGTTCAATCGAAAATTTGATTTATGACCCGGAGCAAAACGAT
Consensus    (1701)  CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C
                      1751                                              1800
      Sh1    (1740)  GAGCACAAGTTCGTGCTGAAGGACAAGAAGAAGCCGATCATCTTCTCGAT
     Sus1    (1720)  GAGCACAAGTTCGTTCTGAACGACAGGAACAAGCCAATCATCTTCTCCAT
     Sus3    (1658)  GAACACATTGGGCATCTGGATGACCGGTCAAAGCCCATCCTCTTCTCCAT
Consensus    (1751)  GAGCACAAGTTCGTTCTGAA GACAGGAA AAGCC ATCATCTTCTCCAT
                      1801                                              1850
      Sh1    (1790)  GGCGCGTCTCGACCGCGTGAAGAACATGACAGGCCTGGTCGAGATGTACG
     Sus1    (1770)  GGCTCGTCTCGACCGTGTGAAGAACTTGACTGGCTGGTGGAGCTGTACG
     Sus3    (1708)  GGCAAGACTCGACAGGGTGAAGAACATAACAGGGCTGGTCGAAGCTTTTG
Consensus    (1801)  GGC CGTCTCGACCG GTGAAGAACATGACAGGGCTGGTCGAG TGTACG
                      1851                                              1900
      Sh1    (1840)  GCAAGAACGCGCGCCTGAGGGAGCTGGCGAACCTCGTGATCGTTGCCGGT
     Sus1    (1820)  GCCGGAACAAGCGGCTGCAGGAGCTGGTGAACCTCGTGGTCGTCTGCGGC
     Sus3    (1758)  CTAAGTGCGCTAAGCTGAGGGAGCTGGTAAACCTTGTCGTCGTTGCCGGG
Consensus    (1851)  GCAAGAACGCGCGGCTGAGGGAGCTGGTGAACCTCGTGGTCGTTGCCGG
                      1901                                              1950
      Sh1    (1890)  GACCACGG---CAAGGAGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA
     Sus1    (1870)  GACCATGG---CAACCCTTCCAAGGACAAGGAGGAGCAGGCCGAGTTCAA
     Sus3    (1808)  TACAATGATGTCAACAAGTCCAAGGACAGGGAAGAGATCGCGGAGATAGA
Consensus    (1901)  GACCATGG   CAAC AGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA
                      1951                                              2000
      Sh1    (1937)  GAAGATGTACAGCCTCATCGACGAGTACAAGTTGAAGGGCCATATCCGGT
     Sus1    (1917)  GAAGATGTTTGACCTCATCGAGCAGTACAACCTGAACGGGCACATCCGCT
     Sus3    (1858)  GAAGATGCATGAACTCATCAAGACCCACAACTTGTTCGGGCAGTTCCGCT
Consensus    (1951)  GAAGATGTATGACCTCATCGAG AGTACAACTTGAACGGGCA ATCCGCT
                      2001                                              2050
      Sh1    (1987)  GGATCTCGGCGCAGATGAACCGTGTCCGCAACGGGGAGCTGTACCGCTAC
     Sus1    (1967)  GGATCTCCGCCCAGATGAACCGCGTCCGCAACGGCGAGCTGTACCGCTAC
     Sus3    (1908)  GGATCTCTGCCCAGACAAACAGGGCCCGTAACGGCGAGCTCTATCGCTAC
Consensus    (2001)  GGATCTC GCCCAGATGAACCG GTCCGCAACGGCGAGCTGTACCGCTAC


                      2051                                              2100
      Sh1    (2037)  ATTTGCGATACCAAGGGCGCATTCGTGCAGCCTGCGTTCTACGAAGCGTT
     Sus1    (2017)  ATCTGCGACACCAAGGGCGCCTTCGTGCAGCCTGCTTTCTACGAGGCTTT
     Sus3    (1958)  ATCGCTGATACCCATGGTGCTTTCGTACAGCCGGCCTTGTATGAAGCGTT
Consensus    (2051)  ATCTGCGATACCAAGGGCGC TTCGTGCAGCCTGC TTCTACGAAGCGTT
                      2101                                              2150
      Sh1    (2087)  CGGCCTGACTGTGATCGAGTCCATGACGTGCGGTCTGCCAACGATCGCGA
     Sus1    (2067)  CGGGCTGACGGTGGTTGAGGCCATGACCTGCGGCCTGCCCACGTTCGCCA
     Sus3    (2008)  CGGTCTCACCGTCGTTGAGGCCATGACCTGTGGGCTTCCTACTTTCGCGA
Consensus    (2101)  CGG CTGAC GTGGTTGAGGCCATGACCTGCGG CTGCC ACGTTCGCGA
                      2151                                              2200
      Sh1    (2137)  CCTGCCATGGCGGCCCTGCTGAGATCATCGTGGACGGGGTATCTGGCCTG
     Sus1    (2117)  CCGCCTACGGCGGTCCGGCCGAGATCATCGTGCACGGCGTGTCTGGCTAC
     Sus3    (2058)  CGCTCCATGGAGGTCCAGCTGAGATCATAGAGCATGGCGTCTCGGGCTTC
Consensus    (2151)  CC  CCATGGCGGTCC GCTGAGATCATCGTGCACGGCGT TCTGGCTTC
```

Figure 9d

```
                     2201                                              2250
      Sh1   (2187)  CACATTGACCCTTACCACAGCGACAAGGCCGCGGATATCCTGGTCAACTT
     Sus1   (2167)  CACATCGACCCTTACCAGGGCGACAAGGCGTCGGCCCTGCTCGTGGACTT
     Sus3   (2108)  CACATTGACCCGTACCACCCCGAACAGGGTGTTAATCTGATGGCCGACTT
Consensus   (2201)  CACATTGACCCTTACCAC GCGACAAGGC GCGGATCTGCTGGTCGACTT

                     2251                                              2300
      Sh1   (2237)  CTTTGACAAATGCAAGGCAGATCCGAGCTACTGGGACGAGATCTCACAGG
     Sus1   (2217)  CTTCGACAAGTGCCAGGCGGAGCCGAGCCACTGGAGCAAGATCTCCCAGG
     Sus3   (2158)  CTTCGACCGGTGCAAGCAAGACCCAGATCACTGGGTGAATATATCTGGAG
Consensus   (2251)  CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG
                     2301                                              2350
      Sh1   (2287)  GCGGCCTGCAGAGAATTTATGAGAAGTACACCTGGAAGCTCTACTCCGAG
     Sus1   (2267)  GCGGGCTCCAGCGTATCGAGGAGAAGTACACCTGGAAGCTGTACTCGGAG
     Sus3   (2208)  CAGGGCTGCAGCGCATATACGAGAAGTACACATGGAAGATATACTCAGAG
Consensus   (2301)  GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG
                     2351                                              2400
      Sh1   (2337)  AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGAGCAA
     Sus1   (2317)  AGGCTGATGACCCTCACCGGCGTGTACGGGTTCTGGAAGTACGTGTCCAA
     Sus3   (2258)  AGGTTGATGACACTGGCCGGGGTCTACGGTTTCTGGAAGTACGTGTCGAA
Consensus   (2351)  AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGTCCAA
                     2401                                              2450
      Sh1   (2387)  CCTGGAGAGGCGCGAGACCCGCCGCTACATCGAGATGTTCTACGCCCTGA
     Sus1   (2367)  CCTGGAGAGGCGCGAGACCCGGCGGTACCTGGAGATGCTGTACGCGCTCA
     Sus3   (2308)  GCTCGAGAGGCTGGAGACGAGGCGCTACCTTGAGATGTTCTACATACTGA
Consensus   (2401)  CCTGGAGAGGCGCGAGACCCGGCGCTACCT GAGATGTTCTACGC CTGA
                     2451                                              2500
      Sh1   (2437)  AGTACCGTAGCCTGGCAAGCCAGGTTCCGCTGTCCTTCGA------TTAG
     Sus1   (2417)  AGTACCGCACCATGGCGAGCACCGTGCCGCTGGCCGTGGA------GGGA
     Sus3   (2358)  AGTTCCGCGAGCTGGCGAAGACCGTGCCGCTTGCAATTGACCAACCGCAG
Consensus   (2451)  AGTACCGCA CCTGGCGAGCACCGTGCCGCTGGCC T GA       G AG
                     2501                                              2550
      Sh1   (2481)  TACGGGGAAAGAAGGAGA-AGAAGAACGAAGAAGCCCAGGCCGGA-----G
     Sus1   (2461)  GAGCCCTCCAGCAAGTGA-TGCGTGACGGCGGCCACAGACCTGATC---G
     Sus3   (2408)  TAGCTTGCGCAACTGCGACTGCGTAGCACTTGGTACAAGACTGAAACCTG
Consensus   (2501)  TAGC   GC AGAA G GA TGCGTAACA   GGCACAGGCCTGA      G
                     2551                                              2600
      Sh1   (2525)  AACCATCGCCTGCATTTCGATCT---------GT-TTCACCGCAATTCGC
     Sus1   (2507)  ATCGATGAGCGAGAGGGAGCACTCGGA-----GT-GTCGTGTCTTTTCCC
     Sus3   (2458)  AAGGACCTTCAGTAATTTAGGCGCGGCAGACGGTAGCCAATAAAATGTGC
Consensus   (2551)  AACGATC   C G A TT G  CTCGG       GT GTCA    CAATTCGC
                     2601                                              2650
      Sh1   (2565)  ATTGTTAGTCGTGTATTGGAGTTATGTG--TACTTGGTTTCCAAGAACTT
     Sus1   (2551)  TTGCCATTTCTTTCTTTCTTCTTTTTCC--TTCCCGGAGGCGAAAAAAAA
     Sus3   (2508)  CGGAGCTGAACTGGTTTTTTATTATGTACATAATGGCAGTATAACAAAAT
Consensus   (2601)   TG    TGTC TG TTT TT TTATGT    TACT GGAGTC AA AAAAT
                     2651                                              2700
      Sh1   (2613)  TGGTTCCTTCTCGTTTTTTTTCCTTGTTTGAGCGTTTTTGGGCAGCGCTG
     Sus1   (2599)  AGAGTC-TGCTT-TTGCTAGGCGGCGGGCGTTCGTTGCTGCTCTTTGCTT
     Sus3   (2558)  TACTGAAGGCAGGTGGGTTGCAGTTGTGTGTTCGTTACTG--------TT
Consensus   (2651)  TG TTC TGCT GTTG TTG CGTTGTGTGTTCGTT CTG  C    GCTT
                     2701                                              2750
      Sh1   (2663)  GCCTGGTTCCTAGTATGGTGGAATTGGCTGCACCTTTTGCTTCGAATAA
     Sus1   (2647)  CAAGAGTTAAAATTTACCTACC--TTGTCAAGGTCTTGTTCCATCATTGA
     Sus3   (2600)  TACTGTATTATGTCAAGCTGTC----GGCTGCAATTTCTTTGCTGG--CA
Consensus   (2701)   ACTGGTT ATATTAAGCTG C  TTGGCTGCA CTT TTC  TGA T A
```

Figure 9e

```
                  2751                                                2800
      Sh1   (2713) AAATGCCTGCTCGTTCACCTGTCTTCCAGAGTGC----------------
     Sus1   (2695) TCCGGGTGTCGCTTGTAGTAGTCTGATGGACTGTTAGTAGTTTGCGTTGC
     Sus3   (2644) AGCCGCAGGCACTGGTGAAGTGCTGATAAATACATCATATTCTGTTGACC
Consensus   (2751) A C GC GGC CTTGTA   GTCTGATAGA TG T  TA T TG     C
                  2801                                                2850
      Sh1   (2747) --------------------------------------------------
     Sus1   (2745) GTCGGTTGAGAGGGAACGTTGGTGGTGGTGGTGTGTGTGCAGTCAGGCGT
     Sus3   (2694) TGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC------
Consensus   (2801)    G    A A   AA                   G G G    C

                  2851                                                2900
      Sh1   (2747) --------------------------------------------------
     Sus1   (2795) GGTGCTCCCTTTGTTTCCTGGATGGGATGTTGCTCCTTGAATAATAATCG
     Sus3   (2738) --------------------------------------------------
Consensus   (2851)

                  2901                                                2950
      Sh1   (2747) --------------------------------------------------
     Sus1   (2845) TAGTGGCCTTGGAGCCCTTTTCCTGAAATAAGAGCAGCATCCTAGTGCTT
     Sus3   (2738) --------------------------------------------------
Consensus   (2901)

                  2951      2964
      Sh1   (2747) --------------
     Sus1   (2895) ACCTTTGCAGCTGT
     Sus3   (2738) --------------
Consensus   (2951)
```

Figure 9f

CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG

CGCGCGCGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCC**ATG**TCTGCCCCGAAGCTGA

ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC

TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA

TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT

TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

Figure 10

Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11

ATGTCTGCCCCGAAGCTGAACCGCAACGCGAGCATCCGG

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

[redacted]g accgcgtcga ggacaccctc cacgcgcacc gcaacgagct 60
cgtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atcctgcagc cgcaccacat 120
cctcgacgcg ctcgacgagg tccagggctc cgggggccgc gcgctagccg agggaccctt 180
cctcgacgtc ctccgctccg cgcaggaggc gatcgtgctg ccgccgttcg tggccatcgc 240
ggtgcgcccg cgcccgggag tttgggagta cgtccgcgtc aacgttcacg agctcagcgt 300
cgagcagctc acagtctcgg agtacctccg cttcaaggag gagcttgtcg acggccagca 360
caatgatccc tacgttctcg agcttgactt cgagccgttc aatgtctcag tcccacgccc 420
aaatcggtca tcatctattg gaaacggtgt gcagttcctc aaccgacact tgtcctcaat 480
catgttccgc aacagggatt gcttggagcc cctgttggat ttcctccgtg gccaccggca 540
caaggggcat gttatgatgc ttaatgatag aatacaaagc ttggggaggc ttcagtctgt 600
gctgaccaaa gctgaggagc acttgtcaaa gctccctgct gacacaccat actcacaatt 660
tgcttataaa tttcaagagt ggggcctgga gaaaggttgg ggtgatacag caggacatgt 720
tttggaaatg atccatctcc ttctagacat cattcaggcg ccagacccat ctaccctaga 780
gaaattcttg ggaggatcc ccatgatttt taacgttgtt gtggtatccc ctcatggata 840
ctttggtcaa gctaatgtat taggcttgcc agacacagga ggacagatcg tctatatact 900
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ggaaacattt gctgaggatg ctgctggtga aattgctgct gaattacaag gtactccaga 1200
cttcataatt ggaaactaca gtgatggaaa tcttgtggcg tcattgctat cttacaagat 1260
gggaattacc cagtgcaaca ttgctcatgc tctggaaaag actaagtatc cagattcaga 1320
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gctggtcgaa gcttttgcta agtgcgctaa gctgagggag ctggtaaacc ttgtcgtcgt 1800
tgccgggtac aatgatgtca acaagtccaa ggacagggaa gagatcgcgg agatagagaa 1860
gatgcatgaa ctcatcaaga cccacaactt gttcgggcag ttccgctgga tctctgccca 1920
gacaaacagg gcccgtaacg gcgagctcta tcgctacatc gctgataccc atggtgcttt 1980
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aaaaaaaaaa aaaaaaaaaa aaaaaaaggg cggccgc

Figure 11